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DEFINITION	Sequence 87 from Patient WO0073469.			

AX056443

VERSION AX056444.1 01:12229150

KRYWICKI'S

Sketch

CHRISTIANISM

REFERENCES

AUTHORS

1113

JOHNNAI,

HEADLINES

.....
SOUTH

.....

BASE CATALYST

DEBATE

C R I M I N A L

Summary

calculated.

—

Probit

ad iugum erit.

17-684

ALVIN

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15 JULY 2004

[illegible][illegible]

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ACCESSION	AK000342
VERSION	AK000342.1 GI:7020362
KEYWORDS	oligo capping; fls (full insert sequence).


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DEFINITION Drosophila melanogaster L123246 full length cDNA.

ACCESSION AY061314

VERSION AY061314.1 GI:16769285

KEYWORDS FLY_CDNA.

SOURCE fruit fly.

ORGANISM Drosophila melanogaster

REFERENCE 1 (bases 1 to 2652)

Slapleton, M., Brokstein, P., Honig, J., Ashburner, A., Carlson, J.,

Champo, M., Chavez, C., Iotsoff, V., Fartman, D., Friso, E., George, R.,

Gonzalez, M., Guarin, H., Li, J., Liang, J., Miranda, A., Murali, C.,

Nunoo, J., Pacle, J., Parag, V., Park, S., Phoumavong, S., Wan, K.,

Yu, C., Lewis, S.E., Rubin, G.M. and Colniket, S.

Submitted (30-Oct-2001) Berkeley Drosophila Genome Project,

Lawrence Berkeley National Laboratory, 140 Cyclotron Road,

Berkeley, CA 94720, USA

Sequence submitted by:

Berkeley Drosophila Genome Project

Lawrence Berkeley National Laboratory

Berkeley, CA 94720

COMMENT

REFERENCE

Slapleton, M., Brokstein, P., Honig, J., Ashburner, A., Carlson, J.,

Champo, M., Chavez, C., Iotsoff, V., Fartman, D., Friso, E., George, R.,

Gonzalez, M., Guarin, H., Li, J., Liang, J., Miranda, A., Murali, C.,

Nunoo, J., Pacle, J., Parag, V., Park, S., Phoumavong, S., Wan, K.,

Yu, C., Lewis, S.E., Rubin, G.M. and Colniket, S.

Submitted (30-Oct-2001) Berkeley Drosophila Genome Project,

Lawrence Berkeley National Laboratory, 140 Cyclotron Road,

Berkeley, CA 94720, USA

Sequence submitted by:

Berkeley Drosophila Genome Project

Lawrence Berkeley National Laboratory

Berkeley, CA 94720

FEATURES

source

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location/Qualifiers

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Seq. name: qb in: A(000,4488)

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At002448				
Protophila melanocephala, chromosome 2R,				
D506886, complete sequence.				

15506888, completed sequence.

VERSION AC0005448.1 01:4818440

SHIRLEY L. LUI Y.

1000

REFERENCE
1 (bases 1 to 86689)

REVISION

Altieri, J. E., Arizumi, A., Arizumi, T., Porter, E., Blazynski, J., Butenhardt, C., Champo, M., Chavez, C., Chow, M., Ciolek, K., Doyle, C. M., Farrant, E., Galio, K., Gierke, R. A., Harris, N. L., Hoskins, R. A., Houston, K. A., Humast, L. S., Katta, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, F., Lomax, M. A., Marada, P., Moschetti, A. R., Moschetti, M., Nixon, K., Parolek, J. M., Park, S., Pfeiffer, B., Poon, L., Punct, E., Sepucha, A., Sethi, H., Solt, E., Sotarsky, K. R., Tway, B., Ware, K. H., Weinburg, L., Zhang, K., Zierman, J., and Kubinski, M.
 Sequencing of *Drosophila* chromosome 2R, region 44A2-44A4 unpublished (1998)

Appendix

JOURNAL,

CO-MM-F-N

Submitted (14 Aug. 1998). Biophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA
on Oct. 4, 1998. This sequence version replaced at: 6805721.
Sequence submitted by:
Berkeley Biophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720

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LOCUS AY060721 1394 bp mRNA linear INV 08-NOV-2001
DEFINITION *Drosophila melanogaster* GH16988 full length cDNA.
VERSION AY060721.1 GI:1676099
KEYWORDS fruit fly
ORGANISM *Drosophila melanogaster*
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephyraidea; *Drosophilidae*; *Drosophila*.
REFERENCE
1. (bases 1 to 1394)
Stapleton, M., Beckstead, P., Honig, L., Abayaratne, A., Carlson, J.,
Champo, M., Chavez, J., Forcett, V., Farfan, D., Friese, R., George, R.,
Gonzalez, M., Martin, H., Lipp, J., Mac, J., Miranda, A., Mungall, C.J.,
Nimmo, J., Parlob, L., Paragas, V., Park, S., Planchetta, S., Wang, K.,
Yan, J., Lewis, S.E., Rubin, G.M. and Kier, S.
Direct Submission
Submitted (30 OCT 2001) Berkeley *Drosophila* Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley *Drosophila* Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
sequence clones from *Drosophila* gene collection 1 (Rubin et al.,
Science 2000). The sequence has been subjected to integrity checks
for sequence accuracy, presence of a polyA tail and contiguity
within 10 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clone. However, there are
artifacts associated with the generation of cDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unsliced precursor RNAs, and
reverse transcription errors that result in single base changes.
For further information about this sequence, including its location
and relationship to other sequences, please visit our web site
(<http://genetics.berkeley.edu>) or send email to
cduffy@berkeley.edu

FEATURES
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BASE COUNT 479 a 413 g 487 t
GIGIN

Alignment Scores:
Quality: 403.00 Length: 428
Ratio: 1.942 Gaps: 14
Percent Similarity: 51.402 Percent Identity: 23.673

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232 G1YTh111111111111111111111111111111111111111 478
458 GCGAG11 507
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749 GAGAACTGAC111111111111111111111111111111111111 798
347 PGLYAsp11111111111111111111111111111111111111 864
799 GGGGGAG1111111111111111111111111111111111111 827
364 e11 869
828 CCA11 877
370 Val111 885
878 ATTCTGAGAT11111111111111111111111111111111111 927
385 o11 902
928 CTGCGT11111111111111111111111111111111111111 977
402 h11 418

[illegible][illegible]

[illegible]

seq_documentation_block:
10 AAC66423 standard; DNA; 1837 BP.

$$A: AA\{6642\};$$

111 14-1443-20001 (first entry)

IDE Human secreted protein coding sequence SFG 10 Nov 24.

KW chemotherapy; endocrine; neoplasms; neuropeptides; neuropeptide Y; and pituitary
antihypertensive; hepatotropic; antidiabetic; and inflammation; and infection;
KW antihepatocellular carcinoma; and immunologic; and immunologic; and parasitic;
KW endocrine; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disorder; infection; human; secreted protein; *hsc*

05 Homo sapiens.

IN W0200058350-A1.

FD-05-OCT-2000.

14- 22-MAR-2000; 2000WO-0507483.

PR 26-MAR-1999; 99US-0126596.

11A (HUMA-) HUMAN GENOME SORTING

PI ROSEN A, KILBEN SM, KOMATSOULIS G

05/25/2007 1:14 PM

Parkinson's diseases and cancers

claim in Page 442; 423pp; English

cc The invention relates to the isolation of genes AAc66410-66458 encoding
cc 49 human secreted proteins AAB32002-332950. The genes can be used to
cc generate fusion proteins by linking to the gene for the human
cc immunoglobulin 3 Fc portion (SEQ101) for increasing the stability of
cc the fusion protein as compared to the human protein only. The genes and
cc proteins are useful for preventing, ameliorating or treating medical
cc conditions, e.g. by protein or gene therapy. The genes are isolated
cc from a range of human tissues disclosed in the specification. The
cc nucleic acids, proteins, antibodies and (anti)agonists are useful in
cc the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
cc and ovarian cancer, and other cancers of the adrenal gland, bone, bone
cc marrow, breast, gastrointestinal tract, liver, lung, or uterine cervix;
cc (b) immune disorders e.g. Addison's disease, allergies, autoimmune
cc haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
cc disease, multiple sclerosis, rheumatoid arthritis and ulcerative
cc colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d)
cc wound healing; (e) neurological diseases e.g. cerebral anoxia and
cc epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
cc and parasitic infections.

Sequence 1837 B2; 539 A, 368 C, 343 G; 586 T; 1 other.

adj_instrument_scores:

Quality:	1595.00	Length:	496
Ratio:	4.834	Steps:	2
Percent Similarity:	66.532	Percent Identity:	65.927

ad iqnme'it_block:

Aliquid Seq 1/1 to: AAC66423 from: 1 to: 1837


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1644 CAGATGGTAAATGCTAAAGGCTTACTTTAAAGCTATCATTCAGACGGCAAG 1683
447 GAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 483
1684 GAGTGGCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1733
444 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
1744 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1783
450 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 486
1784 GAGTGGCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1833
467 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
1844 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1883
480 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 497
1884 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1933
497 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 500
1944 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1983
501 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 516
1984 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2033
516 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 523
2044 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2083
523 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 539
2084 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2130
540 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 552
2144 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2180
552 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 569
2184 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2240
569 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 570
2244 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2285
seq_name: /ST011711.1
seq_documentation_block:
10 ABL05356 standard: cDNA; 4742 bp.
XX ABL05356
XX
XX 20 MAR 2002 (first entry)
XX
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 10550.
XX
XX Drosophila developmental biology cell signaling insecticide?
XX
XX Drosophila melanogaster
XX
XX W0200171042-A2.
XX
XX 27 SEP 2001.
XX
XX 28 MAR 2001: 2001W-0509241.
XX
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PR 23-MAR-2000: 2000US-191637P.
PE 11-JUL-2000: 2000US-0614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW:
XX
XX WPI: 2001-656860/75.
XX
XX P-PSDB; ABB61253.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions -
XX
XX Claim 1: SEQ ID NO 10550; 21pp + sequence listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from drosophila. The invention is
XX useful in developmental biology and in elucidating cell signaling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL01840-ABL01875) and the encoded proteins
XX (ABB5737-ABB72072).
XX
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from WIPO
XX at ftp.wipo.int/pub/published_pat_sequences.
XX
XX Sequence 4742 BP; 1367 A; 1084 C; 1056 G; 1243 T; 0 other;
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alignment_scores:

Quality:	901.50	Length:	761
Ratio:	2.248	Gaps:	19
Percent Similarity:	52.694	Percent Identity:	31.144

alignment_block:

us-09-684-458-2 x ABL05356

Align seq 1/1 to: ABL05356 from: 1 to: 4742

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1472 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1521
51 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 68
1522 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1571
68 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 84
1572 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1621
85 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 101
1622 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1671
101 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 118
1672 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1721
118 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 129
1722 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1771
130 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 141
1772 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1821
141 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 147
1822 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1871
```


[illegible]

1844	CC...ACACCGAATATGCTGTCTGAGGATATGGAGATATGCTATATGCAAT	1890
546	...MetSQTARCTGVALAALoulenSerIleelluASnpheoIlnlyst61	
1891	GAGCCACACGACCTCTGGCTGTCTGAGGATATGGAGATATGCTATATGCAAT	1940
561	YHluouARAllySAlAlystThrolySAsp	570
1941	ATGCTGTGCAAGATGAGATATGCAATATGCAAT	1990
seq_name:	seq_id:	seq_len:
seq_documentation_block:		
1D	AA527387 standard; cDNA; 440 bp.	
AC	AA527387;	
XX		
1F	07-NOV-2001 (first entry)	
XX		
DE	cDNA encoding novel signal transduction pathway protein, Seq ID 422.	
XX		
KW	Neuroprotective; cytoskeletal; dermatological; immunosuppressive; tumour;	
KW	antifibrotic; anti-HIV; antibacterial; anti-inflammatory; cancer;	
KW	immune system disorder; rheumatoid arthritis; inflammatory condition;	
KW	organ transplant rejection; infection; hepatitis; blood disorder;	
KW	atrial cell aneurysm; hypoproliferative disorder; Gaucher's disease;	
KW	neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;	
KW	chromosomal abnormality; twin syndrome; ischemia; renal disorder;	
KW	cardiovascular; respiratory; wound healing; endocrine; Addison's disease;	
KW	reproductive system; gastrointestinal; liver disorder; AIDS; SS;	
KW	acquired immune deficiency syndrome.	
OS	homo sapiens.	
XX		
PN	W0200154733-A1.	
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PD	02-AUG-2001.	
XX		
PF	17-JAN-2001; 2001WO-US01312.	
XX		
PR	31-JAN-2000; 2000005-0179065.	
PR	04-FEB-2000; 2000005-0180628.	
PR	24-FEB-2000; 2000005-0184664.	
PR	02-MAR-2000; 2000005-0186350.	
PR	16-MAR-2000; 2000005-0189874.	
PR	17-MAR-2000; 2000005-0190076.	
PR	18-APR-2000; 2000005-0198123.	
PR	19-MAY-2000; 2000005-0205515.	
PR	07-JUN-2000; 2000005-0209467.	
PR	28-JUN-2000; 2000005-0214886.	
PR	30-JUN-2000; 2000005-0215135.	
PR	07-JUL-2000; 2000005-0216647.	
PR	07-JUL-2000; 2000005-0216880.	
PR	11-JUL-2000; 2000005-0217487.	
PR	11-JUL-2000; 2000005-0217496.	
PR	14-JUL-2000; 2000005-0218290.	
PR	26-JUL-2000; 2000005-0220963.	
PR	26-JUL-2000; 2000005-0220964.	
PR	14-AUG-2000; 2000005-0224518.	
PR	14-AUG-2000; 2000005-0224519.	
PR	14-AUG-2000; 2000005-0225213.	
PR	14-AUG-2000; 2000005-0225214.	
PR	14-AUG-2000; 2000005-0225266.	
PR	14-AUG-2000; 2000005-0225267.	
PR	14-AUG-2000; 2000005-0225268.	
PR	14-AUG-2000; 2000005-0225270.	
PR	14-AUG-2000; 2000005-0225447.	
PR	14-AUG-2000; 2000005-0225757.	
PR	14-AUG-2000; 2000005-0225758.	
PR	14-AUG-2000; 2000005-0225759.	
PR	18-AUG-2000; 2000005-0226279.	
PR	22-AUG-2000; 2000005-0226681.	
PR	22-AUG-2000; 2000005-0226868.	

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24	0.1	SEP	2000	2000.15	-0.229	0.45
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PR	17-NOV-2000;	2000US-0249209.
PR	17-NOV-2000;	2000US-0249210.
PR	17-NOV-2000;	2000US-0249211.
PR	17-NOV-2000;	2000US-0249212.
PR	17-NOV-2000;	2000US-0249213.
PR	17-NOV-2000;	2000US-0249214.
PR	17-NOV-2000;	2000US-0249215.
PR	17-NOV-2000;	2000US-0249216.
PR	17-NOV-2000;	2000US-0249217.
PR	17-NOV-2000;	2000US-0249218.
PR	17-NOV-2000;	2000US-0249244.
PR	17-NOV-2000;	2000US-0249245.
PR	17-NOV-2000;	2000US-0249264.
PR	17-NOV-2000;	2000US-0249265.
PR	17-NOV-2000;	2000US-0249297.
PR	17-NOV-2000;	2000US-0249299.
PR	17-NOV-2000;	2000US-0249300.
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PR	01-DEC-2000;	2000US-0250391.
PR	05-DEC-2000;	2000US-0251030.
PR	05-DEC-2000;	2000US-0251988.
PR	05-DEC-2000;	2000US-0256719.
PR	06-DEC-2000;	2000US-0251479.
PR	08-DEC-2000;	2000US-0251856.
PR	08-DEC-2000;	2000US-0251868.
PR	08-DEC-2000;	2000US-0251869.
PR	08-DEC-2000;	2000US-0251989.
PR	08-DEC-2000;	2000US-0251990.
PR	11-DEC-2000;	2000US-0254097.
PR	05-JAN-2001;	2001US-0259678.
XX		
PA	(HOMA) IRMAN SHIMM 0371 170.	
XX		
PT	Rosen CA, Barash SC, Rubin SM;	
PT	WT1, 2001 465460/50.	
PR	P-PSDB; AA017470.	
XX		
PT	Novel polypeptides useful for diagnosing, treating, preventing and/or	
PT	proposing disorders related to the proteins, including cancers, immune	
PI	disorders and neuronal disorders	
XX		
PS	Claim 1; SEQ ID No 422; 88pp; English.	
XX		
CC	The invention relates to novel isolated polypeptides (I), and	
CC	polynucleotides (II). (I), (II) and the antibody to (I) are useful for	
CC	diagnosing, preventing and treating diseases including immune system	
CC	disorders (e.g. congenital and acquired immunodeficiencies, autoimmune	
CC	disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ	
CC	transplant rejections and graft versus host disease, infectious diseases	
CC	(e.g. hepatitis C), bleeding disorders (hemorrhic abnormalities and	
CC	other blood related disorders (sickle cell anemia), myeloproliferative	
CC	disorders, primary haematopoietic disorders, hypoproliferative	
CC	disorders (e.g. Gaucher's disease and more), neurodegenerative	
CC	disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal	
CC	abnormalities (down syndrome), ischemic injury (e.g. stroke), renal	
CC	disorders (e.g. glomerulonephritis), cardiovascular disorders	
CC	(e.g. arrhythmia), respiratory disorders, neurological disorders, in	
CC	wound healing, epithelial cell proliferation, endocrine disorders (e.g.	
CC	Addison's disease), reproductive system disorders, metastatic	
CC	disorder (inflammatory disorders), liver disorders (cirrhosis),	
CC	as stimulators of B-cell responses, as T cell activators, activators of	
CC	T-cells, to induce higher affinity antibodies, and as a means to induce	
CC	tumour proliferation in pathologies such as regulated immune deficiency	
CC	syndrome (AIDS). AAS24976 AAS27850 proposed novel secretory conductin	
CC	pathway protein coding sequences and PCR primers of the invention.	
XX		

alignment_scores:		
quality:	640.00	104
Ratio:	4.848	345
Percent Similarity:	98.507	Percent Identity: 97.761

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1724	CGTTCAGGAGAAAGAGATGATGCTGCTGCTGGCTGGTGGCTGGCAGATC	1769
441	CGSCTValAspValIleGlySerLeuGlyPheSerLeuGlyArgLeuMetThrTyr	447
1770	CAAGAAATGGAGAAATGGCTGTCTTGGCAATCTGCTGCAAGATGATGGAGCT	1819
447	CTGGATGCTTGGAGSCTValIleProValAspSerProProGluProSer	464
1820	CTTCTATCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1848
564	CTMetAlaValValIleGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln	368
1840	CTATCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1898
560	CTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	381
1890	ATAAAGAAATAAATCTGGAGATATATAGCTTAACTCTTGAAGCGGCTAG	1948
581	SASCTMetSerProGluIleSerArgLeuGlnGlnMetProGluIleSerGln	398
1940	CTTCTCTCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1998
308	SPValIleGluGluThrSerLeuGlySerGluPheGlySerLeuPheThrLeuGly	414
1990	CTATCTATCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2039
415	LeuGlySerLeuAlaGluArgLeuValIleGlnIleGlyIleGlyIleGlyArgGluIle	431
2040	ATTAAATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2054
431	CGTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	448
2054	CTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2054
448	CGTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	464
2065	CTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2084
465	LysGlySerGlySerArgAlaIleGluAsnSerGluGluHisSerAlaArg	481
2095	GTAAAGAGGCTCAAGTGGTCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2105
481	CTTCTCTCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	498
2106	CTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2148
498	CGTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	514
2149	CTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2189
515	ProGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln	518
2190	CTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2239
518	CTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	534
2240	ATAAAGAAATAAAGAAATCTGGAGATATATAGCTTAACTCTTGAAGCGGCTAG	2285
534	CTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	550
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KW Drosophila developmental biology cell regulation insecticide
KW pharmaceutical gene ss
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OS Drosophila melanogaster
PN W020017104Z-A2
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PD 27-SEP-2001
XX
PF 2-MAR-2001; 2001wo-US09231
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PK 23-MAR-2000; 2000us-191637P
PR 11-JUL-2000; 2000US-0614150
XX
(PERE ) PE CORP NY
PA
PI Venter M, Adams M, Li PWD, Myers EW
XX
OR WI, 2001 656860/75,
DR F-PIDB; ABB67608
XX
PT Now isolated nucleic acid detection reagent for detecting 1000 or more
PI genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
PS Claim 1: Seq ID No 29615; Zfp + Sequence List enq, English
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB101840 AB16175) and the encoded protein
CC sequences (AB101840 AB16175) and the encoded proteins
CC (ABR57737-ABR72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 2459 BP; 657 A; 685 C; 601 G; 519 T; 0 other;

alignment_scores:
    quality: 401.00      length: 432
           ratio: 1.823       gaps: 14
Percent Similarity: 50.926   Percent Identity: 29.398

alignment_block:
US 09 684 458 2 x AB1.1711 .

Align seq 1/1 to: AB1.1711 from: 1 to: 2459

145 LYSTPGILValValGlnProLeuIysAsnIleelyl(Fam) OArly 161
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1255 CGTACGAAGTCATGCCACCTGGATTAAATAACTGTGCACCAATCGAAC 1304
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161 STSYTRheLaMetLysIleCysAsnGlnTrpLysLT Andou... 176
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1405 GAATGTTTCTTAACAATAAATCTTGAAAGAAGAAAATCATCAAGAA 1454
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177 .....VallouselHPAdAspleullyro 186
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1455 ATTAGTAACTTAACTGAAATAGTAAAGTAAAGTAAAGTAAAGTAAAG 1464
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186 AsplystyrlouserAsplyAspbhoellYstoufeyystouloupT 202
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1405 AAATATATGCVAGG.....CAAATAATTAAGAGATCTGAGG 1442
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202 OSerCysteullisProTyrlleTyraArgValThr.....PhenA 215
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1443 CTGCTGTCATCTCCGTACATATATATGCTTCTGGACTTCACCTTTTGG 1492
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215 LalrAlaAsrcGluscrSerAlalaoucouleAtdMedfAcscilIndys 231

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[illegible][illegible]

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PD      26-JUL-2001.
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EE      -26-DEC-2000; 200CWO-US34263.
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PR      -21-JAN-2000; 200OHS-0488725.
PR      -25-APR-2000; 200OHS-0552417.
PR      -09-JUL-2000; 200OHS-0598042.
PR      -19-JUL-2000; 200OHS-0620412.
PR      -04-AUG-2000; 200OHS-0654550.
PR      -14-SEP-2000; 200OHS-0662191.
PR      -19-OCT-2000; 200OHS-0694046.
PR      -29-NOV-2000; 200OHS-0727444.
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EA      (HYSE-) HYSEQ INC.
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PI      Tang YT, Lin C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
PI      Wang J, Wang Z, Wehrman T, Xu G, Xue AJ, Yang Y, Zhang JJ
PI      Zhao GA, Zhou P, Goodrich K, Drmanno KI;
XX
XX      WPI; 2001-442253/47.
PR      p-PDB; AAM40620.
XX
P1      Novel nucleic acids and polypeptides useful for treating disorders
P1      such as central nervous system injuries .
XX
PS      Claim 1; SEQ ID NO 3765; 10078pp; English.
XX
CC      The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC      the encoded polypeptides (AAM38642-AAM42213) with neurotropic,
CC      immunosuppressant and cytostatic activity. The polynucleotides are useful
CC      in gene therapy. A composition containing a polypeptide or polynucleotide
CC      of the invention may be used to treat diseases of the peripheral nervous
CC      system, such as peripheral nervous injuries, peripheral neuropathy and
CC      localised neuropathies and central nervous system diseases, such as
CC      Alzheimer's, Parkinson's disease, Huntington's disease, amyotropic
CC      lateral sclerosis, and Shy drager syndrome, other uses include the
CC      utilisation of the activities such as: immune system suppression,
CC      Activin, Endothelin antagonism, treatment of rheumatic activity, haemostatic
CC      and thromolytic activity, cancer diagnosis and therapy, drug screening,
CC      assays for receptor activity, arthritis and inflammation, leukemias and
CC      CNS disorders.
PC      Note: The sequence data for this patent did not form part of the printed
PC      specification.
SC      Sequence 2711 BP; 826 A; 496 C; 572 G; 817 T; 0 other;
XX

alignment_scores:
    quality:   211.50           length:       454
    ratio:     0.900            gaps:        19
Percent Similarity: 51.76% Percent Identity: 21.46%

alignment_block:
US 09-684-458-Z x AAI59776 ...
Align seq 1/1 to: AAI59776 from: 1 to: 2711

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404 TACTGTTAIAAGTTCGTGGlllc AgcggGa.....AcAgglgAAI 64+
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344 GGTTTGCTTCAGAGAAATATGcAGAGTTIGAtAAAA'TITATAAACCTTAA 99+
67 .....GlnldeAlaglylenSerloeprofoendrprolysylslauIl 81
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394 AAAA AACAGTTTCCTCGTAGAGccctGAAGATTCCTGCCAAGAAATATTT 44+

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  id: AAV99653 standard; CDNA; 2512 bp.
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  AC AAV99653;
  xx
  UT 17 MAR 1999 (first entry)
  xx
  DE Human serum glucocorticoid-regulated kinase (h-SGRK2) encoding cDNA.
  xx
  KW Serum glucocorticoid-regulated kinase; h-SGRK2; human; gene therapy;
  KW serine/threonine protein kinase; inflammation; rheumatoid arthritis;
  KW septicemia; autoimmune disease; inflammatory bowel disease; psoriasis;
  KW transplant rejection; infection; stroke; ischemia; renal disorder;
  KW leucenesis; brain injury; acquired immune deficiency syndrome; AIDS;
  KW metabolic; bone; osteoporosis; lymphoproliferation; attherosclerosis;
  KW Alzheimer's disease; cancer; ss.
  xx
  OS Homo sapiens.
  OS
  FH Key location/Qualifiers
  FT CDS 129..1619
  FT /tag= a
  FT /product= "h-SGRK2 polypeptide"
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  PN EP889127-A1.
  xx
  PD 07-JAN-1999.
  xx
  PE 18-JUN-1998; 98EP-0304830.
  xx
  PR 23-DEC-1997; 97US-0997212.
  PR 01-JUL-1997; 97US-0051446.
  xx
  PA (SMK ) SMITHKLINE BEECHAM CORP.
  xx
  PI Kumar S, Zou C;
  PI
  PF WPI 1999 06265876.
  PF P-PSDB; AAW87772.
  DR
  XX New nucleic acid encoding human h-SGRK2 polypeptide(s) useful for
  XX diagnosis, treatment and prevention of e.g. arthritis, infections,
  XX cancer, Alzheimer's disease
  XX
  PS Claim 2; Pages 7-8; 27pp; English.
  PS
  CC This cDNA encodes a human serum glucocorticoid-regulated kinase (h-SGRK2)
  CC polypeptide, a novel member of the serine/threonine protein kinase

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1192 GAAGCAGAACCTTCATGTACTGCAGAGGAGGACACTGACTTTAGAGAG 1244
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1292 CAGGTCAAAGCCTTAGCAGATGCTTATGAATAAGAGAGAGAGAGAGAG 1344
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1342 CAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1375
474 subserGlnHisSerAlaIarAlaYsSerAsnSerAsnAsnSerOlySer 490
1375 ..... 1375
491 GlyAlaSerSerProLeuHisSerPro..... 499
1376 ...GGCGTGAATCCGAGAGAGATGGGTCAATGTCAGAGAGGGRAGATACA 1422
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1523 CTCAGAGCGCTGCTGCACTGCACTGCACTGCTGCTGCTGCTGCTGCA 1572
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seq_name: GenBank: J01375 The DNA sequence of gene 731C-4
seq_documentation_block:
? Sequence 3, Application US/08290731C
? Patent No. 5843646
? CHEMICAL INFORMATION:
? APPLICANT: HOWELL, David Douglas Lawrence
? TITLE OF INVENTION: DNA RECOMBINANT PROTEIN MOBILE
? FILE OF INVENTION: SON OF SEVENTEEN (MSOS) GENE,
? TITLE OF INVENTION: AND METHOD FOR PRODUCING
? NUMBER OF SEQUENCES: 15
? CORRESPONDENT'S ADDRESS:
? ADDRESS: STREET, ROOM, CITY, STATE & ZIP
? STREET: 2100 PENNSYLVANIA AVENUE, N.W.
? CITY: WASHINGTON
? STATE: D.C.
? COUNTRY: USA
? ZIP: 20037
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: Fortran/MS DOS
? SOFTWARE: Patent In Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/082907, 731C
? FILING DATE: 17 OCT 1994
? CLASSIFICATION: 435

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[illegible]

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1 TYPE: nucleic acid
2 STRANDEDNESS: single
3 TOPOLOGY: linear
4 MOLECULE TYPE: cDNA
5 FEATURE:
6 NAME/KEY: Coding Sequence
7 LOCATION: 127...1404
8 US: 08 852-743 1

alignment_scores:
    quality: 150.50      Length: 475
    ratio: 0.681         gaps: 25
    Percent Similarity: 46.526    Percent Identity: 23.368

alignment_block:
US-09-684-458-2 x US-08-852-743-1 ..

Alignment seg 1/1 to: US-08-852 743-1 from: 1 to: 1975

168 11elyAsnclhProLysclhArgleuValleuSerTfAlaAspleu...183
   ||| ||||| ||||| ||||| ||||| ||||| |||||
238 ATCGATACGACACCAAGGAGGTGTGTGGTCAACAGATCAATCGA 287
   ||| ||||| ||||| ||||| ||||| ||||| |||||
184 ...glyProAspLysTyrleuSerAspLysAspIleuTle...199
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288 GGAGGCGGAGGATGAGATC.....GAGGATATTCATGATCA 328
   ||| ||||| ||||| ||||| ||||| ||||| |||||
199 yslleuclhProCysleuHisProLysTleTyrArgValIlePheAla 235
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
329 CTGCTCTCAGTCAGTGGGAGAGCTGTCAATCAATCGATTTGGCTC 378
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
216 ThrAlaSerclhSerAlaIleuIleValArgMetPheAsnclhLyscl 232
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
379 TACCTAAAGAGCATCAAGCTATGGATCATATAGATATCTGGGCGAT 428
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
232 yThrlleuLysAspleuIleTyrLysAlaLysProLysAspIleIleuL 249
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
429 CTCAGCACTGGATTCCT.....AAGCA... 453
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
249 yslLysTyrCysAsnProLysLysIleclhLysleuclhIle 265
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454 .....GGTCCC.....CTGGAGGAGCATATACATT 477
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266 LysThrTyrclhValGlnIleleuclhValleuLysPheleuHisAspLy 282
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
478 GCGACGATGCTCGAGGAGATCTGAGAGGCTGGATATATCTATCTCGCA 527
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
252 sclYpheProTyrclhLysleuHisAlaSerAsnValMetleu...A 297
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528 AGCGAAGATCGACGAGACATCAAAATCTGCAGCTGTACTCTCGGAGT 577
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297 spclYAspThrTyrArgleuLeuAspleu... 306
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578 AAGATGATGTTT...AAGATGATGATAATTGATATGATGATATCA 624
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607 .....clhAsnclhValleuclhLysleuclhLysleuclhLysleuclh 618
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625 GACACGACAGATTAAAGGAAATCTCTGGGATATCTGGAAT 671
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318 gSerTyrPheSerclhPheArgLysIleAsnThrleuclh...SerValA 334
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
672 GGGAT...CTGAGGATATCAATAGAGAGTGAATATTAAGGCTG 715
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
334 spValHisCysPheclhLysleuclhLysleuclhLysleuclhLysleuclh 350
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716 ACATCTGGATCTTGGATATCAATATCGAGTGGATAGAGAGGCTT 765
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351 ProAspSerValProValAspSerPheProProAlaProSerMetAlaVa 367
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766 CCAAACTCT...GACCTCTATCTC...ATCGAGCT 794
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467 lValAlaValleuclhSerThrleuSerTyrclhAlaLysLysAsnclhLym 484

```


[illegible]

1001 Commonwealth Blvd., Suite 1000
 Cambridge, MA 02142
 Tel: 617/552-4000
 Fax: 617/552-4006

```

GENERAL INFORMATION
ADDITIONAL WILLIAM TULL MCGEE
ADDITIONAL TELETYPE NO. 6201600 IS
ADDITIONAL DAVID SHAY SHERWOOD
TITLE OF INVENTION HUMAN STRESS LIKE STRESS ACTIVATED
TITLE OF INVENTOR RICHARD ALBERT KINASE
FILE REFERENCE NUM 70272
CURRENT ADDITION NUMBER 89-07-0001-1-6
CURRENT EDITION DATE 1998-09-14
BRIEF ABSTRACT ADDITION NUMBER 9719920.2
PUBLICATION DATES 1997-09-19
NUMBER OF FIGURES 1
DRAWINGS PROVIDED FOR WINDOWS VERSION 3.0
FIGURE NO. 1
TEXT DATA
ABSTRACT
TECHNICAL ABSTRACT Sequence
REMARKS
OTHER INFORMATION Additional Information
of 1997-10-01

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[illegible]

Accepted for publication: 05.09.1996

[illegible][illegible]

1890 CAGAGAAATTTAAAGTGGGCAACCTCTTGGCTTTTCAAGCATGGGTAAGCTGA 1844

[illegible]

889 rgleLuglmetProLeuthesetAspValLeuLeuInTheSeoCln 405
 : : : | | | | : : : | : : : :
 1594 GAACTTACACTAAACCTCTTAACGATTTCTGGAGGCTGTGTTAAATAAG 1545

406 LysProGlnIlePheLysIleProThrLysLeuLysGluAlaLeuArgLeuA 422
 ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
 1544 GAGCCGAGCTTAA...GTAAAT.....GG 1522

[illegible]

.
.
.

[illegible][illegible]

seq_name: qb_est1:Al.557856

seq_documentation_block:

LOCUS	955 bp	mRNA	linear	EST	16-DEC-2003
DEFINITION	AL557856	LT1_HNF008_Tc2 Homo sapiens cDNA clone (S01J004YF6.5)			

prime, mRNA sequence

VERSION A1.557856.1 01:12301867

South Pole human.

Fukaryota; M

REFERENCES

Full-length cDNA libraries and normalization

Journal: *Biopulsations* (2001)
 Comment: Contact: Genoscopy

BP 191 91006 EVRY Cedex France

Panel 1: Sequential microscope images

Summary

10.1016/j.neuroscience.2010.08.022

Issue_Type

was primed with a Not I-colligo (dT) primer. P1

colored into the Not I and Pco RV sites of the p^WMS^{Pro}okl in

Life Technologies, Contact : Perkin Elmer Life Technologies,

Rockville, Maryland 20850, USA Fax : (1) 410 610 8477

BASE COUNT	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726
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[illegible]

seq_name: qb_est2:BM463267

Set-Definition

DEFINITION A.1. Let $\mathbf{A} \in \mathbb{R}^{n \times n}$ and $\mathbf{B} \in \mathbb{R}^{n \times m}$. Then, the matrix $\mathbf{A} + \mathbf{B}\mathbf{B}^T$ is called the *augmented matrix* of \mathbf{A} .

ACCESSION HM463267

KEYWORDS

CHRISTIANISM Homo sapiens

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

AUTHORS NIH-MGC <http://mgs.nih.gov/>

JOURNAL Unpublished (1999)

Email: cqapbs-rc@mail.nih.gov
 Tissue procurement: ATOT

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library: Arrived by The I.M.A. of Fort Collins (IN)

DNA Sequencing by: Agencourt Bioscience Corporation
 Clones distributed by: Millipore Corporation

Found through the J.M.A.T.F. Consortium, mff/jlnn at:
mff@cam.ac.uk

High quality sequence spot: 604
Plate: LAM2352 row: 0 column: 02

100041036/Chia 11 1975

"I don't know"

Colonel, Major, 10 0024
Colonel, 11th "Ninth" 92

7. Issue - type of work (e.g., "field work")

Site 2: Salt-tolerant indigenous and planted primed.

average length of 16.6 characters and consisted of 1000 randomly generated characters. The length of the characters was determined by the technologies available at the time of the study.

[illegible]

01101011

alignment_scores:

Ratio: 4.665

05-01 684 458 2 X B3463267

Altitude: 509 m; Date: 1946.3.26; From: 1 to 112

[illegible][illegible]

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seq_id:documentation_block:
locus: AL558573 884 bp mRNA linear EST 16-FEB-2001
DEFINITION: AL558573.111.NT1008.T02 Homo sapiens cDNA clone GSDJ006Y118.5
prime, mRNA sequence.
ACCESSION: AL558573
VERSION: AL558573.1 GI:12903224
KEYWORDS: EST.
SOURCE: human.
ORGANISM: Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE:
1 (bases 1 to 884)
Li, W.B., Gruber, C., Jessop, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL:
CONTACT: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91106 EVRY CODEX - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
FEATURES:
location/Qualifiers

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/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone "GSO1006YJ18"
 /clone_1db "J11_NF008_1G2"
 /sex="male"
 /tissue_type "T cells from T cell leukemia"
 /note "Vector: pMV360R1.6; Site: 1. Not 1st strand cDNA
 was primed with a NotI oligo(dT) primer, five prime end
 enriched, double stranded cDNA was digested with NotI and
 cloned into the NotI and EcoRV sites of the pMV360R1.6
 vector. Library was normalized. Library was constructed by
 life technologies. Contact: Penn Land Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax: (1) 301 610 8671
 Email: jlana@lifetech.com URL:
<http://www.lifetech.com>"

alignment_scores:		
Quality:	1495.50	Length: 288
Ratio:	5.169	Gaps: 1
Percent Similarity:	93.750	Percent Identity: 93.750
alignment_block:		

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72	AlGGCCCTTCATCGAGAAACCTGCACACCGCAAGAGHGTGGTGAACGAAC	122
17	rvalProLeuthrAlaAlaIlevaluaIasercylInsrlLeuclInsrlHisI	34
122	GGTGGCGTTGAACAGTAGCATTCAGAGAGAATAACAAGTGTACTAAGTGTGTAATTCTCATA	172
34	hrnIufyrIleIleArqValGlnArqGlYIieserValGluAsnSerIhp	50

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo; Hominidae; Homo.

REFERENCE
1 (bases 1 to 875)
Li, W.B., Gruber, C., Josses, J. and Polley, S.L.
Full-length cDNA libraries and normalisation
unpublished (2001)

AUTHORS
JOURNAL

COMMENT
Genoscope - Centre National de Séquençage
BP 101 91056 Evry cedex France
Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr

FEATURES
source location/Qualifiers
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/sex="male"
/tissue_type="T cells from T cell leukemia"
/note="Vector pMWScap1.2 derived. Restrict endonuclease was primed with a NotI site. Five times and enriched, double stranded cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pMWScap1.6 vector. Library was normalized. Library was constructed by ligo technologies. Contact: Fred Liang Ligo Technologies, a division of Invitrogen 9603 Medical Center Drive Rockville, Maryland 20850 USA Fax: (301) 514-6100 Email: fliang@ligo.com URL: http://fulllength.invitrogen.com"

BASE COUNT 224 a 192 c 204 t 252 g 8 others

ORIGIN

alignment_scores:
quality: 1258.50 Length: 876
Ratio: 4.955 Gaps: 1
Percent Similarity: 99.219 Percent Identity: 97.056

alignment_block:
US 09 684 458 2 x AL580361.7cov ..

Align seq 1/1 to reverse of: AL580361.7cov 1 to 876

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875 CTTAAGTAGATTCAGGTCTTGAACTCCAGAAAATAAAGTATGGACG 827

270 acnntleacuaValoutyStbelomhisASflysclvctcfrcltyr 287
|||||
820 GAAAAATATAGAGGATCAGAGCTTCATAGAAAGATATCAATTATAG 777

287 lyhlslchHisAlusotASuVALMetIszVpdllyagThlvYAAscy 304
|||||
776 GGATCTTCAGGCTCGCAATGCATGCTCATAGGCTAAATTCvctcTG 727

304 LeuASPlcuGlUAASoSLenluGbyvlenccosetHavLAAscy 320
|||||
726 CTGAGCCTTGAGAATTCTTATTGGGCTTCCTTTCTTCTAACCACTTA 677

320 rPhSeSerglnPheArlyslloasnthLauglusovVAIASPVahisG 337
|||||
676 TTCTTACAATTAGGAATCAAFATATTAAGATTTATATTTACT 627

337 ystHeclYhlslaukautyrctumetThrtvLYAdptdrASPso 354
|||||
626 GTTTGGCCATTAGGTATGAAATGATTATTAATGATGATAGAGTGG 577

554 ValProValASpocPheofrovalatrcosetMetAVALtyVALva 370
|||||
576 GTGGCTGTGAGCTCTTGGCTCTGGGCTGAGAGCTCTTATTTCT 527

370 HouglsuThrleuSerCyslAluGyLvsAsctlyMcpvclHf 387
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Accession	Gene	Species	Chromosome	Position	Orientation	Length (bp)	EST ID	EST Date
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U00002	homo sapiens	homo sapiens	1	100000000	+	1000	U00002	1990
U00003	homo sapiens	homo sapiens	1	100000000	+	1000	U00003	1990
U00004	homo sapiens	homo sapiens	1	100000000	+	1000	U00004	1990
U00005	homo sapiens	homo sapiens	1	100000000	+	1000	U00005	1990
U00006	homo sapiens	homo sapiens	1	100000000	+	1000	U00006	1990
U00007	homo sapiens	homo sapiens	1	100000000	+	1000	U00007	1990
U00008	homo sapiens	homo sapiens	1	100000000	+	1000	U00008	1990
U00009	homo sapiens	homo sapiens	1	100000000	+	1000	U00009	1990
U00010	homo sapiens	homo sapiens	1	100000000	+	1000	U00010	1990
U00011	homo sapiens	homo sapiens	1	100000000	+	1000	U00011	1990
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U00013	homo sapiens	homo sapiens	1	100000000	+	1000	U00013	1990
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U00015	homo sapiens	homo sapiens	1	100000000	+	1000	U00015	1990
U00016	homo sapiens	homo sapiens	1	100000000	+	1000	U00016	1990
U00017	homo sapiens	homo sapiens	1	100000000	+	1000	U00017	1990
U00018	homo sapiens	homo sapiens	1	100000000	+	1000	U00018	1990
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U00026	homo sapiens	homo sapiens	1	100000000	+	1000	U00026	1990
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U00032	homo sapiens	homo sapiens	1	100000000	+	1000	U00032	1990
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U00034	homo sapiens	homo sapiens	1	100000000	+	1000	U00034	1990
U00035	homo sapiens	homo sapiens	1	100000000	+	1000	U00035	1990
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U00037	homo sapiens	homo sapiens	1	100000000	+	1000	U00037	1990
U00038	homo sapiens	homo sapiens	1	100000000	+	1000	U00038	1990
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U00041	homo sapiens	homo sapiens	1					

adaptor: 607A03A0). Size selected (500bp for average insert size 1.8kb). Library constructed by Lund Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

BASE COUNT 192 a 155 c 171 g 202 t
ORIGIN

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Ratio: 5.026 Gaps: 2
Percent Similarity: 97.095 Percent Identity: 97.095

alignment_block:
US 09-684-458-2 x BE270976/rev ..

Align seq 1/1 to reverse of: BE270976 from: 1 to: 720

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202 ProSerCysLeuHisProTyrTleTyrArValThrPheAlaThrAlaAs 218
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218 nGluSerSerAlaLeuLeuTleArgMetPheAsnGluLysGlyThrLeu. 235
|||||
668 TCAATCTCAAGAGTACCTAACTAACTAACTAACTAACTAACTAACTAA 619
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235 ysAspLeuTleTyrLysAlaLysPheLysAspProPheLysLysTyr 251
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618 AGCATCTCATTAACAAGGCTAAATCAAAATAAATCAATCTTAACAAGCTAC 570
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569 TCGAACCCGACAGAGATTCAAGGCTTGGAACTCCACCAATAAAATAAACATA 520
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268 TClYAqClolLolGluValLeuLysPheLeuHisAspLysCTyPheP 285
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519 TCGACGGCAAAATATTAGAGTACCTAACTTCTTCAAGAACAGGATTC 470
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285 rOlyrGlYHisLeuHisAlaSerAsnValMetLeuAspGlyAspThrCys 301
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469 CTATAGGCATCTTCAGGCTCGAACTGCACTCATAGGCTAACTAGCTGC 420
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302 ArgLeuLeuAspLeuGluAsnSerLeuLeuGlyLeuProSerPheCTyAr 318
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419 CGGCTGCTGGAGCTTGAAGATTCCTTATCGGCTGCTTCTTCTTCTACCG 370
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318 qSerTyrrPheSerGluPheArgLysTleAsnThrLeuGluLeuSerValAspV 335
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669 ATCTTATTTTCACAAATTACGAAATCAATATATCTAAATTCGCAATG 320
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335 aHisGlyPheGlyHisLeuLeuTyrGluMetThrTyrGlyArgProPro 351
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319 TCGACTGCTTGGGACCTACCTGATGAAATGACTATAGGACAACTAACTA 270
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352 AspSerValProValAspSerPheProPheAlaProSerMetAlaValVa 368
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368 lAlaValLeuGluSerThrLeuSerCysGluAlaLysLysAsnGlyMetP 385
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219 GAGCTGTGTGGACTTACGCTGCTCTTGAAAGCTCTTAAAAATAGCATGC 170
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418 dLeuArgLleAlaLysGluLysLleLeuLysArgLeuLleGluGluGlu 434
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Revised edition of the 1992
National Institutes of Health, mammalian gene collection (MGC)
distributed (1999)

[illegible]

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Email: c9apbs.r@mail.nih.gov
Tissue procurement: ATCC/CRL-7171/TP
cDNA library preparation: ligo "photon screen, Inc."
cDNA library Arrayed by: The L.M.A.R.C. Consortium (LMB)
DNA Sequencing by: Incyte, Germany
Clone distribution: Map clone distribution information can be
found through the L.M.A.R.C. Consortium/LML at:
http://image.llnl.gov
plate: LLAM9764 row: 1 column: 0
High quality sequence set: 704
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    /lab_host "Inluc (Pharmacia Resistant)"
    /note "Organic Skin Cell Culture Spont. Site 1; Not a
Site 2; Salt model and not fully polymorphic
Average insert size 2 kb. Library constructed by ligo
Technologies."

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3	AAACAACTATCCGGCAACATACAGAGATCCCTGGAAAGATTCCA	52	
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53	IGITCTTCGATCAGAAACAAAGTGGAGGAGGAGAGAGATTGAAATAC	102	
155	LEGLYTPArgIleAlaLysLysTyrPheLeuMetLysLeuLysASP	171	
103	ATAGTTGAGAAATACGCAACAATAATTTTAAATAAATATAAAAATCA	152	
171	nProLysGluArgLeuValLeuSerTTPAAAsTouTyrProASP	198	
153	GGVAAAGGAGCGCTACGTTAAGTGGGCGAATCTGCAAGTAACT	202	
188	YrLeuSerASP	204	
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205	LeuHSPProTyrThrTyrArgValThrPheAlaThrAAsnHSPSerSo	221	
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221	TAAlaLeuLeuLeuArgMetPheAsnGluLysGlyThrLeuLysAspLeu	298	
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288	LeTyrLysAlaLysTyrLeuLysAspTyrThrLysTyrLysAspPro	254	
353	TCTATTAAGGCAAAACCAAAAGAGCATTTCTAAATAAATATTTGAGGCT	402	
255	LysLysTLeuGluGluGluLeuIleuIleLysThrTyrTyrArgGlu	271	
403	AAATAAATTTTACGGCTCTGAGCTTACGTAATTAATAAATATATGAGCA	452	
271	nIleLeuIleValLeuLysTLeuLysThrLeuHSPAspLysTyrProTyrTyrVal	298	

Accession	Gene	Species	Length	EST
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U00002	hprt	Homo sapiens	1000	1000
U00003	hprt	Homo sapiens	1000	1000
U00004	hprt	Homo sapiens	1000	1000
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alignment_scores:	
quality:	1001.00
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percent_similarity:	98.253
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length:	229
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alignment_block:

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17	rValProLeuThrAlaAlaIleGlnAlaSerGlnSerLeuGlnSerHisT	34
106	GCGTCCTGCTGACACAGCTAACCAGGCTAACCTTAGACTTGGCTACA	155
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156	CAGAAATAATATTGAGTGCACAAACAGTAATTTCTGGAAAACGTGG	205
51	GlnIleValArgArqTyrSerAspPheAspLeuAsnAsnSerLeuGl	67
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67	nIleAagIylLeuSerLeuProLeuProLeuLysLysLeuIleLysAsnM	84
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406	GTTTTAGCATCCAAACACCTATCTCCGAAACTATACCTGACATTCCTTGC	455
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bioRxiv preprint doi: <https://doi.org/10.1101/186111>; this version posted June 7, 2002. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

Alignment Statistics:
 Length: 232
 Gaps: 5
 Percent Identity: 92.672

Alignment Score: 44

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